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TECH CENTER 1600/2900



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/537,710B

DATE: 07/31/2002

TIME: 10:02:37

Input Set : A:\EP.txt

Output Set: N:\CRF3\07312002\I537710B.raw

```

3 <110> APPLICANT: Dahlqvist, Andres
4      Stahl, Ulf
5      Lenman, Marit
6      Banas, Antoni
7      Ronne, Hans
9 <120> TITLE OF INVENTION: A new class of enzymes in the biosynthetic pathway for the
production
10      of
11      triacylglycerol and recombinant DNA molecules encoding these enzymes
13 <130> FILE REFERENCE: BASFnae337799PCT1-15
15 <140> CURRENT APPLICATION NUMBER: US 09/537,710B
17 <141> CURRENT FILING DATE: 2000-03-30
19 <150> PRIOR APPLICATION NUMBER: EP 99106656.4
20 <151> PRIOR FILING DATE: 1999-04-01
22 <160> NUMBER OF SEQ ID NOS: 31
24 <170> SOFTWARE: WordPerfect version 6.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1986
28 <212> TYPE: DNA
29 <213> ORGANISM: Saccharomyces cerevisiae
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(1983)
35 <400> SEQUENCE: 1
37 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
38 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
39 1 5 10 15
41 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
42 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
43 20 25 30
45 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
46 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
47 35 40 45
49 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
50 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
51 50 55 60
53 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
54 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
55 65 70 75 80
57 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
58 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
59 85 90 95
61 ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336
62 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe

```

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63	100	105	110	
65	gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384		
66	Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val			
67	115 120 125			
69	ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432		
70	Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn			
71	130 135 140			
73	tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480		
74	Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly			
75	145 150 155 160			
77	aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528		
78	Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val			
79	165 170 175			
81	atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576		
82	Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile			
83	180 185 190			
85	gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624		
86	Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp			
87	195 200 205			
89	gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672		
90	Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp			
91	210 215 220			
93	ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720		
94	Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn			
95	225 230 235 240			
97	ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768		
98	Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile			
99	245 250 255			
101	gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816		
102	Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile			
103	260 265 270			
105	ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864		
106	Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu			
107	275 280 285			
109	gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912		
110	Ala Tyr Leu Asp Leu Glu Arg Asp Arg Tyr Phe Thr Lys Leu Lys			
111	290 295 300			
113	gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960		
114	Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu			
115	305 310 315 320			
117	att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008		
118	Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp			
119	325 330 335			
121	gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056		
122	Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val			
123	340 345 350			
125	aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc	1104		
126	Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly			
127	355 360 365			

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1152
129 gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc
130 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
131 370 375 380
1200
133 att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca
134 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
135 385 390 395 400
1248
137 aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca
138 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
139 405 410 415
1296
141 atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct
142 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
143 420 425 430
1344
145 tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att
146 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
147 435 440 445
1392
149 cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg
150 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
151 450 455 460
1440
153 aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa
154 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
155 465 470 475 480
1488
157 aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa
158 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
159 485 490 495
1536
161 gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg
162 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
163 500 505 510
1584
165 gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac
166 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
167 515 520 525
1632
169 ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat
170 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
171 530 535 540
1680
173 gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct
174 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
175 545 550 555 560
1728
177 gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca
178 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
179 565 570 575
1776
181 atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga
182 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
183 580 585 590
1824
185 att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat
186 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
187 595 600 605
1872
189 ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc
190 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
191 610 615 620
1920
193 gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat

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194 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
195 625                      630                      635                      640
197 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
198 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
199                      645                      650                      655
201 atg ccc ttc cca atg taa 1986
202 Met Pro Phe Pro Met
203                      660
206 <210> SEQ ID NO: 2
207 <211> LENGTH: 661
208 <212> TYPE: PRT
209 <213> ORGANISM: Saccharomyces cerevisiae
211 <400> SEQUENCE: 2
212 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
213 1                      5                      10                      15
215 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
216                      20                      25                      30
218 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
219                      35                      40                      45
221 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
222 50                      55                      60
224 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
225 65                      70                      75                      80
227 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
228                      85                      90                      95
230 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
231                      100                      105                      110
233 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
234                      115                      120                      125
236 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
237 130                      135                      140
239 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
240 145                      150                      155                      160
242 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
243                      165                      170                      175
245 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
246                      180                      185                      190
248 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
249                      195                      200                      205
251 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
252 210                      215                      220
254 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
255 225                      230                      235                      240
257 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
258                      245                      250                      255
260 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
261                      260                      265                      270
263 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
264                      275                      280                      285

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```

266 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
267      290                      295                      300
269 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
270 305                      310                      315                      320
272 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
273                      325                      330                      335
275 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
276                      340                      345                      350
278 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
279                      355                      360                      365
281 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
282      370                      375                      380
284 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
285 385                      390                      395                      400
287 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
288                      405                      410                      415
290 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
291                      420                      425                      430
293 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
294                      435                      440                      445
296 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
297      450                      455                      460
299 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
300 465                      470                      475                      480
302 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
303                      485                      490                      495
305 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
306                      500                      505                      510
308 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
309                      515                      520                      525
311 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
312      530                      535                      540
314 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
315 545                      550                      555                      560
317 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
318                      565                      570                      575
320 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
321                      580                      585                      590
323 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
324                      595                      600                      605
326 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
327      610                      615                      620
329 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
330 625                      630                      635                      640
332 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
333                      645                      650                      655
335 Met Pro Phe Pro Met
336      660
340 <210> SEQ ID NO: 3

```

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2363
Seq#:7; N Pos. 601,627
Seq#:7; Xaa Pos. 116,121
Seq#:9; N Pos. 15,45,83,103,107,112,210
Seq#:25; N Pos. 240,385
Seq#:25; Xaa Pos. 41,89
Seq#:26; N Pos. 601,627
Seq#:26; Xaa Pos. 116,121
Seq#:28; N Pos. 15,45,83,103,107,112,210

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

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L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340
L:658 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:662 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:384
L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:552
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:612
L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:60
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:180
L:2277 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:215
L:2292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:263
L:2303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:359
L:2304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:402
L:2327 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:2357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:384
L:2368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:552
L:2370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:612
L:2409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:2410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:60
L:2412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:180